P. Jacobson

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/915,659*

1652

DATE: 03/13/98
TIME: 16:59:20

INPUT SET: S24140.raw

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

```
 1
 2
 3   (1)    General Information
 4   (i)APPLICANT:  O'Brien et al
 5   (ii)TITLE OF INVENTION:  Novel Extracellular Serine Protease
 6   (iii)NUMBER OF SEQUENCES:  10
 7   (iv)CORRESPONDENCE ADDRESS:
 8   (A)ADDRESSEE:  Benjamin Aaron Adler, Ph.D. J.D.
 9   (B)STREET:  8011 Candle Lane
10   (C)CITY:  Houston
11   (D)STATE:  Texas
12   (E)ZIP:  77071
13   (v)COMPUTER READABLE FORM:
14   (A)MEDIUM TYPE:  1.44 Mb floppy disk
15   (B)COMPUTER:  Apple Macintosh
16   (C)OPERATING SYSTEM:  Macintosh
17   (D)SOFTWARE:  Microsoft Word for Macintosh
18   (vi)CURRENT APPLICATION DATA:
19   (A)APPLICATION NUMBER:  08/915,659
20   (B)FILING DATE:  August 21, 1997
21   (C)CLASSIFICATION:  435
22   (vii)PRIOR APPLICATION DATE:
23   (A)APPLICATION NUMBER:
24   (B)FILING DATE:
25   (viii)ATTORNEY/AGENT INFORMATION:
26   (A)NAME:  Benjamin Aaron Adler, Ph.D.
27   (B)REGISTRATION NUMBER:  35,423
28   (C)REFERENCE/DOCKET NUMBER:  D6020
29   (ix)TELECOMMUNICATION INFORMATION:
30   (A)TELEPHONE:  (713) 777-2321
31   (B)TELEFAX:  (713) 777-6908
32
```

ERRORED SEQUENCES FOLLOW:

```
      312   (2) INFORMATION FOR SEQ ID NO:7:
      313   (i) SEQUENCE CHARACTERISTICS:
-->   314   (A) LENGTH:  260 amino acids
      315   (B) TYPE:  amino acid
      316   (C) STRANDEDNESS:
      317   (D) TOPOLOGY:  linear
      318   (ii) MOLECULE TYPE:
```

INPUT SET: S24140.raw

```
319  (A) DESCRIPTION:  protein
320  (iii) HYPOTHETICAL:  no
321  (iv) ANTI-SENSE:  no
322  (v) FRAGMENT TYPE:
323  (vi) ORIGINAL SOURCE:
324  (vii) IMMEDIATE SOURCE:
325  (viii) POSITION IN GENOME:
326  (ix) FEATURE:
327  (x) PUBLICATION INFORMATION:
328  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:    7:
329  Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu
330                   5           10               15
331
332  Leu Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu
333                   20          25               30
334
335  Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro
336                   35          40               45
337
338  Trp Gln Ala Ala Leu Phe Gln Gly Gln Leu Leu Cys Gly Gly
339                   50          55               60
340
341  Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys
342                   65          70               75
343
344  Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn
345                   80          85               90
346
347  Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro
348                   95          100              105
349
350  His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp
351                   110         115              120
352
353  Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys
354                   125         130              135
355
356  Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln
357                   140         145              150
358
359  Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu
360                   155         160              165
361
362  Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro
363                   170         175              180
364
365  Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly
366                   185         190              195
367
368  Met Val Cys Als Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly
369                   200         205              210
370
371  Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile
```

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/915,659*

INPUT SET: S24140.raw

```
372                    215                   220                   225
373
374    Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly
375                    230                   235                   240
376
377    Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile
378                    245                   250                   255
379    Ile Gly Ser Lys Gly
380                    260
381
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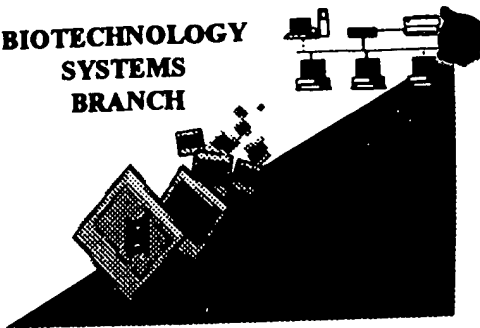
SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/915,659*

DATE: 03/13/98
TIME: 16:59:30

INPUT SET: S24140.raw

Line	Error	Original Text
314	Entered (260) and Calc. Seq. Length (259) differ	(A)LENGTH: 260 amino acids
368	Wrong Amino Acid Designator	Met Val Cys Als Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln

Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CRF 1.821 through 1.825).
Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

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The software can be accessed/requested from the following locations:

1) Dial-up access through the Internet. Location is ftp://ftp.uspto.gov
   The software is in current directory: pub/checker/
   Download all the files. Cost: Free-of-charge

3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
   WASHINGTON DC 20231

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